

# Model assisted phenotyping of rice response to vegetative drought: case study of a collection of 203 tropical japonica genotypes



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**Context:** Drought impact on plant early vigour limits its establishment, resource acquisition and thus final yield. This is a major issue for rice crop, in particular in upland ecosystems. The response of rice early vigour to drought is complex as it involves numerous traits. These traits regulate water and carbohydrates source (assimilation, water uptake) and sink (tillering, developmental rate, leaf size, growth, transpiration) relations (Luquet *et al.* 2008). Japonica group has a great partially unexploited genetic diversity of adaptation to drought and should provide favorable alleles to this traits.

**Objective:** Using a combined approach based on plant modelling and sugar analysis, we phenotype the regulation of water and C source-sink relations by a vegetative drought. We present here the first experimental results and modeling applications

## Materials and Methods

- Greenhouse experiment (CIRAD, Montpellier, France)
- 203 tropical japonica cvs.
- 3 replications (temporal)
- 2 treatments: dry-down/ irrigated
- 11 pots (no rooting differences)



- Drought onset by dry-down when leaf 6 appears (FTSW'=1).
- Transpiration & stress monitored by gravimetry.
- Morphological measurements at FTSW= 1 and FTSW= 0.2: 1<sup>st</sup> leaf size, seed dry weight, tiller and leaf number, haun index, last formed leaf size, final shoot dry weight, and sugar (soluble, starch) contents at FTSW=0.2.



\*FTSW: Fraction of Transpirable Soil Water

## Modelling application

- Description of a response pattern to FTSW using a two-segment model.
- Optimization with Ecomeristem (Luquet *et al.* 2006): model of water and C source-sink processes controlling rice vegetative morphogenesis under drought.

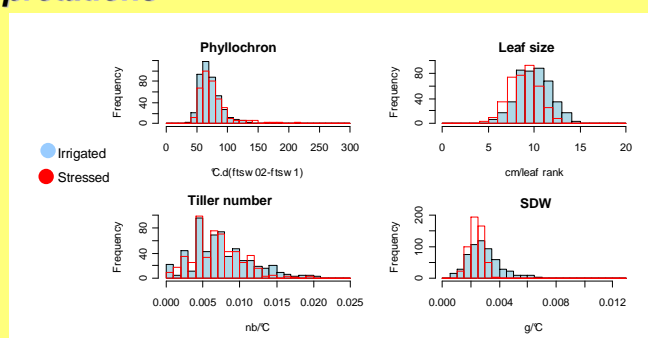
## Results and Interpretations

### Genotype distribution for four measured variables

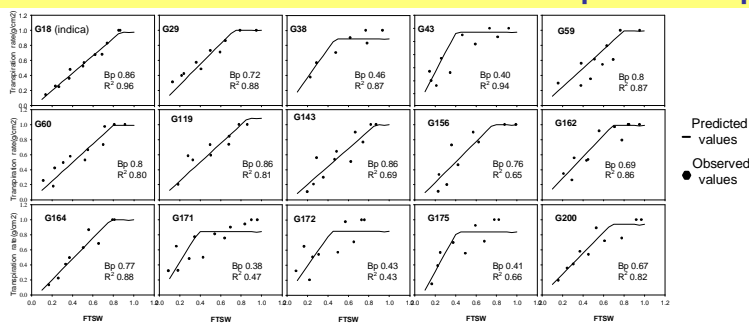
- Water stress affects final shoot dry weight (SDW) through:
  - Changes in developmental rate (phyllchron, tiller number),
  - Changes in organ size (last ligulated leaf size).

- ANOVA on 203 genotypes for 7 variables shows genotype, treatment, and (temporal) replication effects.

- Measured variables show genotypic variation in morphological responses to drought.



### One curve model of normalized leaf transpiration response to FTSW



- Application to 15 genotypes and two repetitions.

- Breakpoints varied from 0.4 to 0.85 across genotypes: Eg. G59 with a higher value than G43 is less able to maintain a higher transpiration during the drying cycle.

- Two-segment models illustrate varietal differences in the control of transpiration.

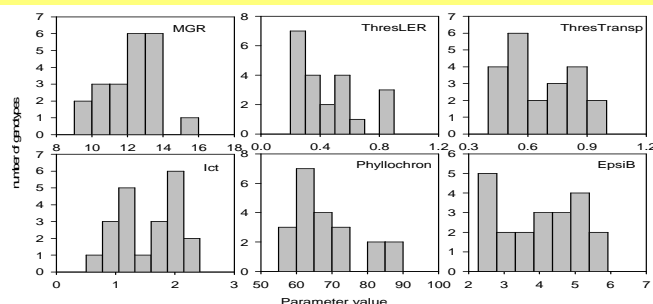
### EcoMeristem model: water and C source-sink processes controlling rice vegetative morphogenesis under drought

- Component traits (parameter values) optimized for genotype discrimination on 21 genotypes:

- Significant range of values (need to enlarge the range for ThresLER),
- No significant correlation between EcoMeristem parameters

- These parameters are both describing physiological processes and genotypic variability.

MGR: Meristem Growth Rate  
ThresLER: FTSW threshold for leaf expansion reduction  
ThresTrans: FTSW threshold for transpiration reduction  
lct: Carbon supply/demand ratio  
Phyllo: Phyllochron  
EpsiB: Conversion coefficient



## Perspectives

Two-segmented regression and model optimization are promising methods to dissect genotype discrimination parameters, the application on the 203 genotypes is underway. We will associate morphogenetic and physiological process-based parameters with sugar contents in source and sink organs to discriminate genotypes. We also want to perform a genetic association study using available SNP markers (2011) to determine markers and alleles of interest for rice response to drought.

**References:** Luquet D., Dingkuhn M., Kim, Tambour L., Clément-Vidal A. Functional plant biology, 33 (4) : 309-323.

Luquet D., Clément-Vidal A., Fabre D., This D., Sonderegger N., Dingkuhn M. 2008. Functional plant biology, 35 (8) : 689-704.